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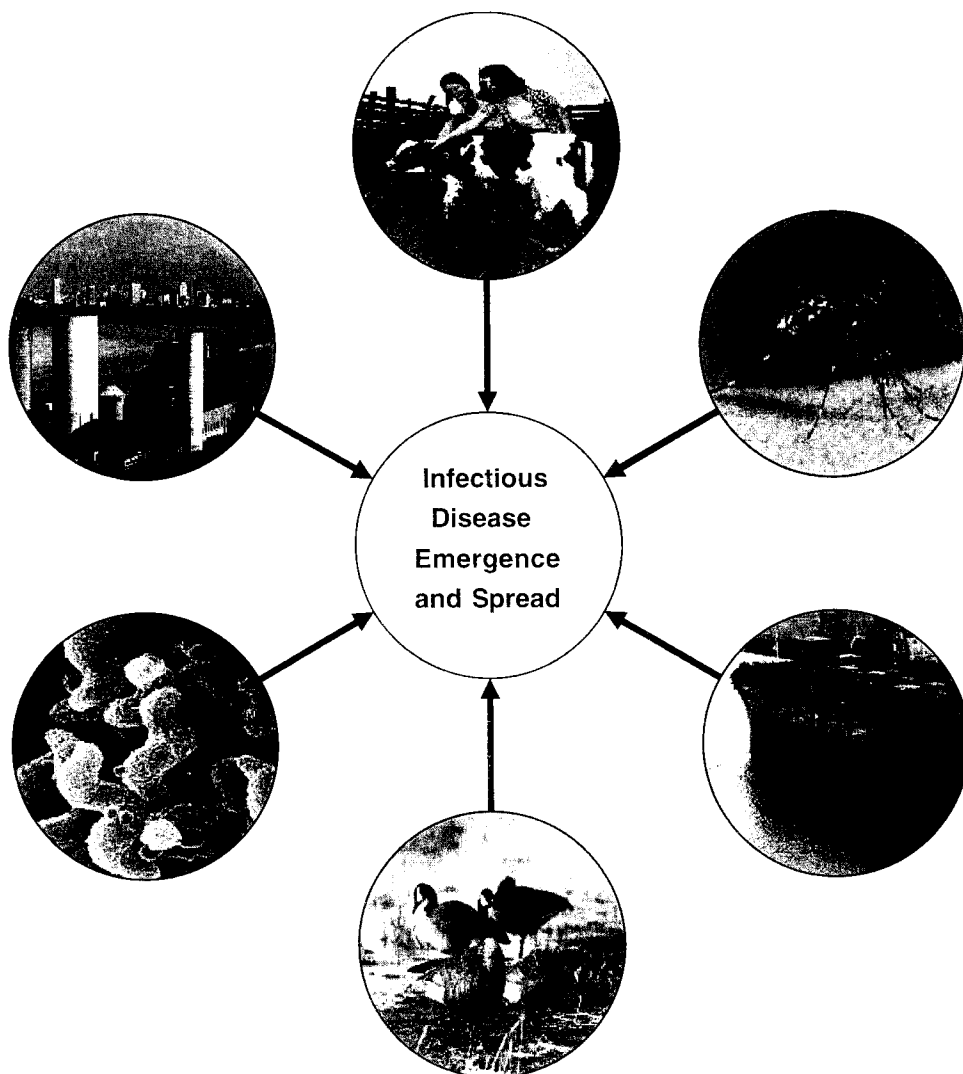
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Overview of Predictive Infectious-Disease Modeling



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INTRODUCTION

PREDICTIVE INFECTIOUS-DISEASE MODELS

Infectious disease emergence is a complex and dynamic process involving biologic, environmental, social, economic, and other factors. Predictive infectious-disease models are used to understand and anticipate disease emergence and predict the time, size, and spatial spread of a disease epidemic. Decisionmakers use predictive infectious-disease models to prepare for and potentially prevent epidemics, plan and evaluate disease control strategies and methods, and allocate resources. During an epidemic, however, decisions should be based on the most accurate information possible from the epidemic rather than on the output of a model with hypothetical inputs.

Given the broad range of modeling objectives, model types, and methodologies available, organizations interested in model development to anticipate disease emergence can use this report for strategic planning. First, this report discusses important considerations for developing predictive infectious-disease models. Next, the report provides a brief overview of model types and methodologies used to predict known and new (previously unrecognized) infectious diseases of animals and humans. Finally, it describes examples of early warning systems utilizing models.

Important Considerations for Development of Predictive Infectious-Disease Models

Predictive models can be classified in several different ways. *Strategic* models yield broad generalizations, have wide applicability, and describe qualitative behaviors (Puccia et al. 1994). Strategic models are useful when the

current state of knowledge is inadequate for precise parameter measurements and when the scope of the question being asked is global or crosses disciplinary boundaries. For example, the model that emerging diseases result from the interaction of the many biologic, environmental, social and economic emergence factors (described on p. 11) is a strategic model.

In contrast, *tactical* models give precise results and rely on specific information, detailed knowledge, and accurate measurements. Tactical models tend to yield practical information that can guide specific intervention efforts. The nasal bot fly model (described on p. 8) is a good example of a tactical model. The bot fly model uses precise soil-temperature data to pinpoint a specific date when bot fly larvae will emerge from pupal cases. The best approach for a complex situation, such as the emergence of new diseases, may be to combine strategic and tactical modeling.

Another way to classify predictive infectious-disease models is into mathematical or statistical model types. Complex models may integrate the use of both mathematical and statistical approaches into a single model. Mathematical models focus on simulating the dynamics of a disease agent's life cycle, including the process of disease transmission as it progresses through a host population in time and space, and therefore, are also known as process-based, mechanistic, disease-transmission, disease-spread, or population models. There is a mathematical relationship between the variables in the model based on knowledge of the underlying biophysical

mechanisms, thus the term mathematical model. For example, the changing numbers of susceptible, infected, and immune hosts in a population over time can be estimated using differential calculus.

Statistical or empirical models focus on the search for a statistical relationship between factors through the statistical analysis of a data set for a defined population. Examples of factors potentially having a statistical relationship with disease incidence include characteristics of the host, such as age or sex, and characteristics of the environment, such as landscape or climate. Those factors having a statistically significant relationship or association with a disease are often called “risk factors.” Two factors being compared statistically could also be disease incidence rates at different time periods.

The limitations of models must be kept in mind. A model is a representation of a real system and is usually a simplification of that system. Models must be validated with data not used in their construction to establish to what extent they behave similarly to the real system they are modeling. Also, disease emergence models should make biological sense. Sensitivity analysis of a model is necessary to determine the sensitivity of the model’s output to poor-quality data and to known variability in system parameters. A model that is highly sensitive to a parameter for which the data are of poor quality should not be used in decisionmaking. Decisionmakers should keep in mind the quote attributed to George Box that “all models are wrong, but some models are useful” (Taylor, 2003).

Answering the following questions will facilitate the development of predictive infectious-disease models.

- **Why? Determine the primary objective for developing the model.**

The type of model selected will depend on the objective or purpose for the model. A process-based model is most effective if the objective is to predict the transmission and spread of a specific disease. An associative-based model, such as the risk-factor model, is most effective if the objective is to determine the attributes of the disease host and the environment that alter the probability of acquiring disease.

- **What? Determine the disease or outcome of interest and the predictive factors likely to be associated with the outcome.**

Quantitative modeling methods require the selection of a dependent outcome variable, which is usually a specific disease. Sufficient and reliable data about the incidence of the disease is needed for statistical modeling. The independent variables (predictors) must be researched and selected, and reliable data must be available.

- **Where? Determine study area and scale.**

A specific geographic area of interest must be defined. Data on the dependent and independent variables of interest must be available in the entire area and at the same scale. This is especially important for models based on risk mapping.

- **When? Determine time period of interest.**

Two time periods must be determined, one that looks to the future and one that looks to the past. The “future” time period relates to the predictive objective and whether the goal is a short-term or long-range forecast. The “past” time period relates to the historical data available on the dependent and independent variables needed to create and test a valid model.

- **How? Determine specific analytical methods.**

The analytical methods implemented will depend on the type of model selected and the type of data available.

- **Who? Determine who will benefit and what actions could be taken using the model results.**

The information produced by the model should be validated, useful to relevant decisionmakers, and linked to response initiatives. Short-term forecasts are useful in helping health services prepare for increased case numbers, whereas long-term forecasts are useful for strategic control of disease. The value of the early warning, both in human and economic terms, should be determined.

INFECTIOUS DISEASE MODELING OBJECTIVES AND MODEL TYPES

OBJECTIVE: PREDICT DISEASE SPREAD DURING AN EPIDEMIC

Many types of mathematical analytic methods can be used to model disease spread in a population, including matrix and network methods. However, models that employ differential calculus methods have been more commonly used and are particularly suitable for diseases transmitted by the direct mode (i.e., animal to animal) (Thrusfield 1995). The SEIR model is a popular modeling framework utilizing differential calculus methods (National Research Council 2001) (fig. 1). SEIR is considered a “compartment” or “state-transition” model because it divides the host population into four compartments or groups of different states. The initial letter of each compartment forms the name of the model:

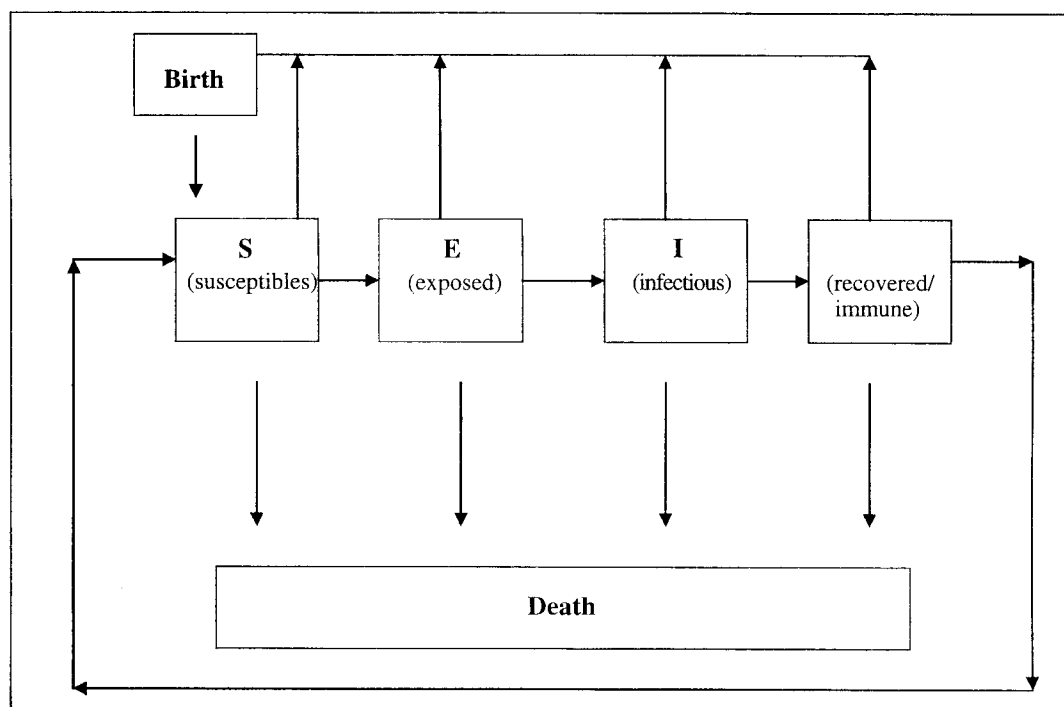
1. Susceptibles (S)—the group susceptible to infection;
2. Exposed (E)—the group exposed to an infectious agent but not yet infectious;
3. Infectious (I)—infectious group; and
4. Recovered (R)—the group recovered, immune, or dead.

The mathematical analytic method used for SEIR modeling involves a series of differential equations that describe the rate of change from

one compartment or state to another as a function of the relative proportions in each compartment. Other disease- and population-specific parameters determined from laboratory and field observations are part of the model, such as the transmission rate and the average duration of infection and immunity (National Research Council 2001). The rate of contact between infectious and susceptible population groups and the transmission rate determine the rate of going from the susceptible to the infected categories. A stochastic component can be added to the SEIR model to incorporate random variation and chance (King and Sorkolne 1988). A spatial component also can be added to the model.

Another important parameter for epidemic mathematical modeling is the basic reproductive number, defined as the number of secondary infections produced by the first infective individual to appear in the population (Dobson and Foufopoulos 2001). A basic reproductive number of less than 1 indicates that the epidemic can not be sustained. A basic reproductive number higher than 1 indicates that an epidemic will continue.

Figure 1—SEIR model framework. (Adapted from National Research Council 2001.)



SEIR modeling has been used to predict the spread of animal diseases such as foot-and-mouth disease (FMD) and classical swine fever, and human diseases such as measles and influenza.

For example, in 2001, SEIR epidemic modeling was used during the FMD epidemic in the United Kingdom to predict disease spread and rank the potential effects of different interventions on the spread of FMD (Ferguson et al. 2001, Keeling et al. 2001).

To simulate an FMD epidemic in the United States, Schoenbaum and Disney (2003) created a stochastic state-transition model that includes spatial and economic components. This model can be used to evaluate alternative mitigation strategies and their epidemiologic and economic consequences. A disease-spread simulation

model for FMD known as InterSpread (Sanson 1993) was developed originally in New Zealand and adapted for FMD in the European Union. InterSpread also has been adapted to model classical swine fever (CSF) in the European Union (Jalvingh et al. 1999).

Disease-spread models are used to prepare and plan for potential epidemics and examine various control strategies in “what if” situations. After reviewing the use of models for establishing disease-control policies during the 2001 FMD epidemic in the United Kingdom, Taylor (2003) concluded that tactical decisions during epidemics should be based on field data and not on complicated simulation models, which may not accurately reflect the true situation on the ground. After an epidemic is over, disease spread models are useful for retrospective analysis to improve knowledge of epidemic behavior.

OBJECTIVE: PREDICT WHEN AND WHERE AN EPIDEMIC OF A KNOWN DISEASE WILL OCCUR IN AN ENDEMIC AREA

To predict when and where a new epidemic of a known endemic disease will occur, past patterns or trends in disease incidence are identified and projected into the future (Myers et al. 2000).

For endemic diseases, mathematical SEIR-type models can be used to forecast the time and size of epidemic recurrences. Statistical modeling approaches also are available to predict endemic disease epidemics.

Three of the most common statistical approaches are time-series, algebraic, and regression models (Nobre and Stroup 1994). Time-series models compare historical data (usually disease incidence) to current data, using the correlation structure of the data. Algebraic models estimate expected numbers of cases based on past cases and compare these to actual observations. Regression models investigate the causal or risk factors related to an epidemic. Other statistical approaches include an exponential smoothing forecasting system, whereby a tracking signal statistic is computed to indicate when the process is different from past observation, and Bayes' Theorem-based methods, which provide distinctions between the epidemic state and the nonepidemic state. A stochastic component to incorporate random variation and chance can be added to models, as appropriate.

To compare and contrast the ability of the models to predict epidemics, Cliff and Haggett (1993) applied data from measles epidemics in Iceland to eight different model types. They found that no single model accurately predicted

both epidemic recurrences and epidemic size. Models that performed well at predicting time of recurrence tended to overestimate outbreak size; models that accurately predicted outbreak size failed to predict time of recurrence accurately. However, adding time-varying parameters, spatial lead-lag structures, and local small-area data on susceptible populations helped alleviate these problems.

A time-series model known as the Autoregressive Integrated Moving Average was used by Watier et al. (1991) to define an alert threshold for foodborne *Salmonella* epidemics (*S. bovis* *morbificans*) in France. To determine an alert threshold for influenza epidemics in Belgium, Snacken et al. (1992) used a regression model that compared observed values for a determined period with expected values and adjusted for seasonal variation and secular trends. Zeng et al. (1988) used Bayes' Theorem methodology to create a model to predict epidemic meningitis in China.

When detailed information is available on the geographic location of cases, spatial models can be used to predict endemic disease epidemics. Incidence mapping is used to show the geographic distribution of disease, and a temporal component can be included as well. Individual cases (case event data) can be mapped, or individual cases can be counted and ascribed to a defined geographic area, such as a county. Mapping of standardized disease rates can indicate geographic differences in disease risk and allow comparisons of disease risk

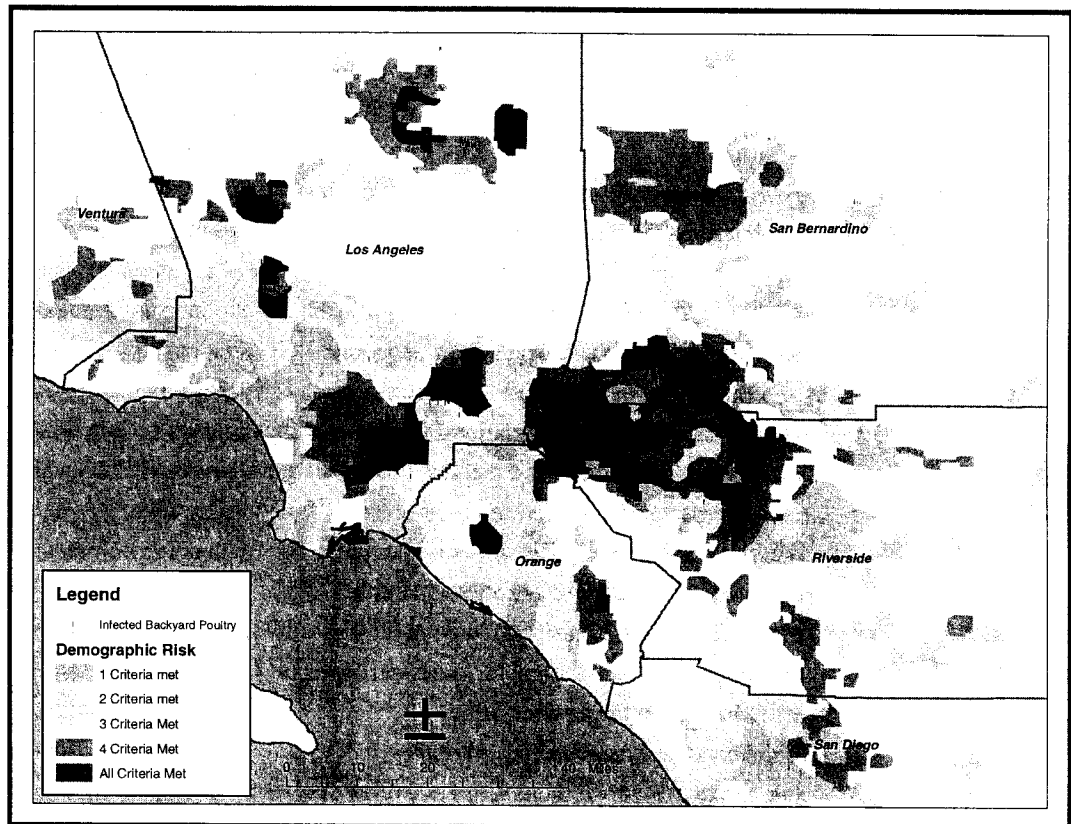
across geographic areas. To standardize disease rates, however, data on the population at risk must be available. Disease mapping can identify “hot spots” but does not answer the question as to why the hot spots occurred in a particular location.

Ecologic risk-map modeling is a spatial method used to identify risk factors that might indicate why a hot spot has occurred in a particular location. Various potential risk factors—such as environmental, demographic, or economic information—can be related to geographic disease-incidence data. Relationships between these predictive factors and the disease-incidence data can be used to predict risk in areas without current disease. For example, during the U.S. 2002–03 exotic Newcastle disease (END) epidemic, risk-map modeling was used to predict geographic areas at risk for END infection (Freier et al. 2004). In California, five demographic variables (population density, ethnic distribution, median home value, population under 17, and median household size) differed significantly among

areas affected with END and areas unaffected. These variables (criteria) were used to rank the likelihood of whether or not areas had backyard poultry (fig. 2). In addition, the risk-map model used variables such as proximity to animal feed stores and poultry suppliers, and zoning code violations such as excess poultry, illegal bird fights, and noisy birds, to make predictions about areas with infected premises.

Biological risk maps focus on biological relationships among organisms during the period leading to disease epidemics. This model has been used primarily for vector-borne diseases such as malaria, dengue, and Rift Valley fever (RVF) and diseases such as hantavirus pulmonary syndrome and plague, which are associated with rodent populations. Climatic, environmental, and ecologic factors affecting vector populations are used to predict disease risk. Biological risk-map models can combine both mathematical (population dynamics) models with statistical (risk factor) models.

Figure 2—Results from a risk model for END based on demographic characteristics in southern California in 2003. (*Adapted from Freier et al. 2004.*)



Often, data on environmental and ecologic factors are obtained through remote-sensing satellites. For example, in Namibia the emergence of nasal bot fly larvae from pupal cases is directly dependent on the number of degree-days that the soil is above a particular threshold temperature. Soil-temperature data received from satellites are used to predict the emergence of bot flies (which infect small stock), allowing farmers in high-risk areas to treat their livestock with larvicides at the most opportune time (Flasse et al. 1998).

Remote-sensing data combined with geographic information-systems modeling have been used to predict epidemics of RVF, a mosquito-borne disease that affects domestic animals and humans in East Africa. RVF epidemics follow periods of widespread, heavy rainfall, which create habitats for the transovarially infected *Aedes* mosquito eggs. Linthicum et al. (1999) found that a model using Pacific and Indian Ocean surface temperature anomalies—coupled with normalized-difference vegetation-index data from satellite photography—could predict RVF epidemics in East Africa up to 5 months in advance.

OBJECTIVE: PREDICT WHEN AND WHERE A KNOWN DISEASE WILL OCCUR IN A NONENDEMIC AREA

Information gained from disease models on explanatory or predictive factors in endemic areas can be used to look for similar patterns and factors in nonendemic areas. For example, mapping vector distributions and environmental factors can help predict which geographic areas are at risk for vector-borne disease spread.

Baylis et al. (2001) used satellite imaging data to predict areas around the Mediterranean that were at risk for bluetongue, by modeling the distribution of the bluetongue vector *Culicoides imicola*.

Geographic information systems (GIS) and spatial analysis tools have been used to identify the range of environmental conditions in Africa that support the bont tick (*Amblyomma hebraeum*), a major vector of heartwater disease in ruminants (Joy et al. 2004). Two modeling methods were used: stepwise decision-tree classification and logistic regression. The environmental variables associated with bont-tick habitat in Africa included elevation, temperature, and precipitation. Using this information, U.S. areas at risk of bont-tick introduction were modeled. Both the classification-tree and the logistic models predicted that the bont tick could survive in parts of 29 States, the majority of which were in the Pacific Northwest.

However, results did differ between the two models. The classification-tree model targeted parts of the upper Midwest and the Northeast, whereas the logistic model targeted parts of the southern and eastern coastlines.

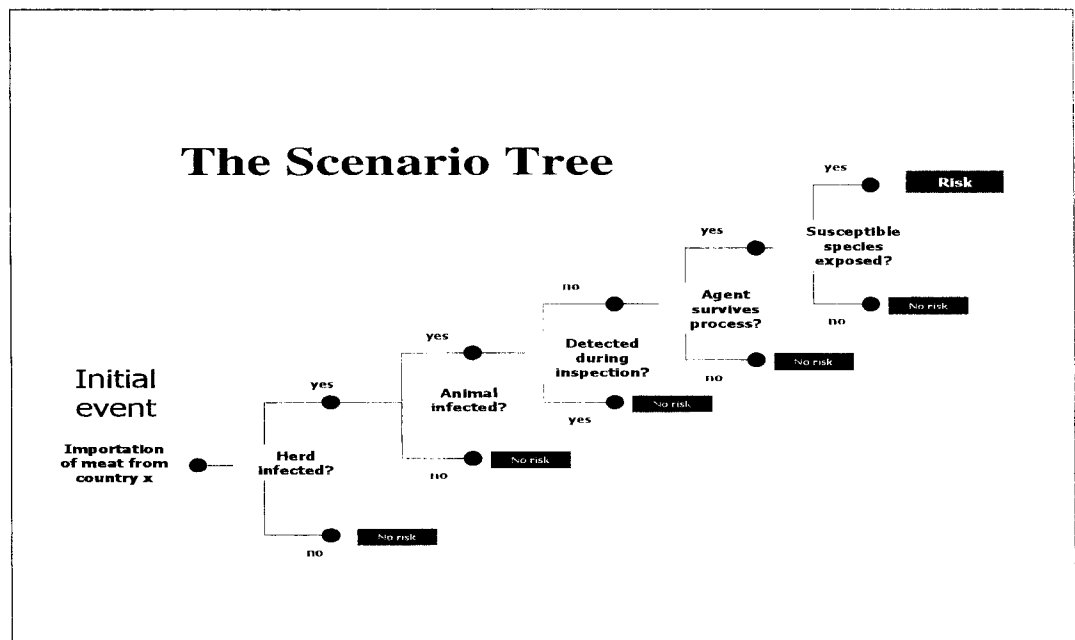
The risk assessment model (a.k.a. risk analysis model) is also used to predict disease spread. This model focuses on specific pathways of pathogen introduction. Risk assessment is often used to evaluate the risk of disease introduction from imported animals or animal products; it is used commonly by regulatory officials in importing countries, including the United States. The first step in risk assessment is hazard identification, which involves identifying the pathogenic agents associated with the importation of an animal or commodity. In addition, risk assessments often conduct pathways analyses, systematic assessments of the pathways in which exotic disease agents might be introduced. Pathways analyses require knowledge of the agent's biology and distribution; import source and quantity of risk products; emigration and tourist flow; and the production and distribution systems of the livestock industries at risk (National Agricultural Biosecurity Center Consortium 2004).

The quantitative analytic method used commonly for this type of risk assessment is likelihood estimation based on conditional probabilities using scenario trees (fig.3). Scenario trees outline each step a pathogen would take in its path from exporting country to importing country, with a probability assigned to each step. Data on disease incidence in the exporting country, diagnostic test sensitivity and specificity, and other relevant data such as agent survivability, are used to determine probabilities. These probabilities are then

multiplied to arrive at the risk of introduction associated with the specified pathway. Risk-reduction steps such as inspection and quarantine can be introduced into the model. For example, Yu et al. (1997) created a risk assessment model to assess the introduction of FMD from the importation of 100 tons of deboned beef. Results of the simulation model showed that the probability of FMD virus

introduction was a function of the prevalence of infected herds, the prevalence of infected cattle in a herd, and the number of cattle selected from a herd. The probability of failing to detect FMD with risk-reduction procedures—such as farm-level inspection, antemortem and postmortem inspection, and chilling and deboning—also impacted the probability of introduction.

Figure 3—Scenario tree for risk of disease introduction from imported meat. (*Adapted from Miller et al. 1993*)



OBJECTIVE: PREDICT WHEN AND WHERE A NEW DISEASE WILL OCCUR

Many previously unrecognized infectious diseases of animals and humans have been identified in the past decade. Most of these diseases are zoonotic. Diseases such as severe acute respiratory syndrome (SARS), Nipah virus, and postweaning multisystemic wasting syndrome have spurred interest in investigating the conditions or factors under which new infectious diseases emerge and spread. Experts in various fields, such as infectious disease, epidemiology, and ecology, have cited the need for complex and integrated models that would predict the emergence of new diseases (Wilson et al. 1994).

Modeling the emergence of a new disease requires a different approach from that used for a known disease because historical incidence data on the new disease do not exist. To date, research has focused on identifying, understanding, and modeling the factors potentially related to new disease emergence, not on predicting where and when an outbreak of a new disease will occur. A better understanding of what factors are associated with the emergence of new diseases could lead to interventions to prevent their occurrence.

The following factors were identified in the Institute of Medicine's 2003 report "Microbial Threats to Health" (Smolinski et al. 2003) as contributing to disease emergence.

Microbial adaptation and change—Microbes, the agents of infectious disease, are continually under selective pressure to adapt through structural and functional genetic changes to

ensure their survival. These genetic changes often allow microbes to "evade" the host's immune system and may allow them to infect new types of hosts (cross the species barrier).

Host susceptibility to infection—The host's ability to evade infection is dependent on many factors, such as genetics, nutrition, previous or current infections, health status, and stress level.

Climate and weather—The geographic distribution and seasonal variation of many infectious diseases indicate that climate and weather have an affect on disease agents and vectors. Disease agents and vectors are sensitive to temperature, moisture, and other ambient environmental conditions determined daily by weather conditions and over long time periods, by climate. Weather and climate also may affect host behavior and susceptibility and impact ecosystems.

Changing ecosystems—Ecologic changes can result in environmental changes, which in turn alter pathogen transmission patterns. Microbial agents that spread by water, air, food, or vectors or that have an animal reservoir are particularly sensitive to changes in environment and ecosystem. Ecologic changes may lead to increased or decreased populations of disease reservoirs and vectors.

Economic development and land use—Human activities result in changes to the physical environment and often impact an area's ecology. Environmental changes resulting from human activities include deforestation,

reforestation, and changes to water and land bodies as a result of dam building. Land-use changes include cutting down forests for agriculture or urbanization. These environmental changes can impact replication of pathogens and may bring new opportunities for contact between hosts and agents. For example, RVF emerged in Senegal after the opening of the Diama Dam, which created additional breeding grounds for mosquitoes.

Human demographics and behavior (social and cultural)—Many current trends in population characteristics promote disease emergence. Increased population size and density provide more opportunities for disease transmission. An aging population and increases of immunocompromised individuals due to chemotherapy, chronic diseases, or human immunodeficiency virus (HIV) lead to more disease-susceptible hosts. Social and cultural dietary practices can promote high-risk behaviors, such as consumption of raw or undercooked meat. The virus that causes SARS is suspected of transferring from animals to humans in the live-animal markets of Guangdong, China. In these markets, many types of live domestic and wild animals are brought together for slaughter to meet the preferences of consumers (Normile and Enserink 2003). In the United States, the trend in exotic pet ownership led to the first U.S. outbreak of monkeypox virus among pet prairie dogs and humans.

Technology and industry—Technological advances can have positive and negative impacts on disease emergence. On the positive side, new technology can lead to improved

living conditions and therefore better health for humans and animals. Technology can result in improved diagnosis and control of disease. On the negative side, technology can provide new avenues for disease transmission, such as through organ and tissue transplantation. Technology can provide new ecologic niches for microbes. For example, the bacteria responsible for Legionnaires' disease adapted to air-conditioning cooling towers.

Changes in the livestock industry and in animal husbandry practices have the potential to impact disease transmission. The trend toward larger farms and increased animal density per farm creates more opportunity for disease transmission and the potential for environmental impacts due to the production of large amounts of manure and waste. Alternatively, large industrial farming operations can play a role in reducing disease transmission risk through disease control programs, greater control over animal movement, and biosecurity practices.

International travel and commerce—As people, animals, animal products, and disease vectors (e.g., mosquitoes, ticks, rodents) move around the world, a major pathway for the spread of infectious human, animal, and zoonotic diseases is created. History abounds with examples of disease emergence related to human migration and animal trade, such as the spread of plague, smallpox, and FMD, and more recently, RVF and SARS.

Societal and technological changes over the last century have led to enormous increases in travel and trade.

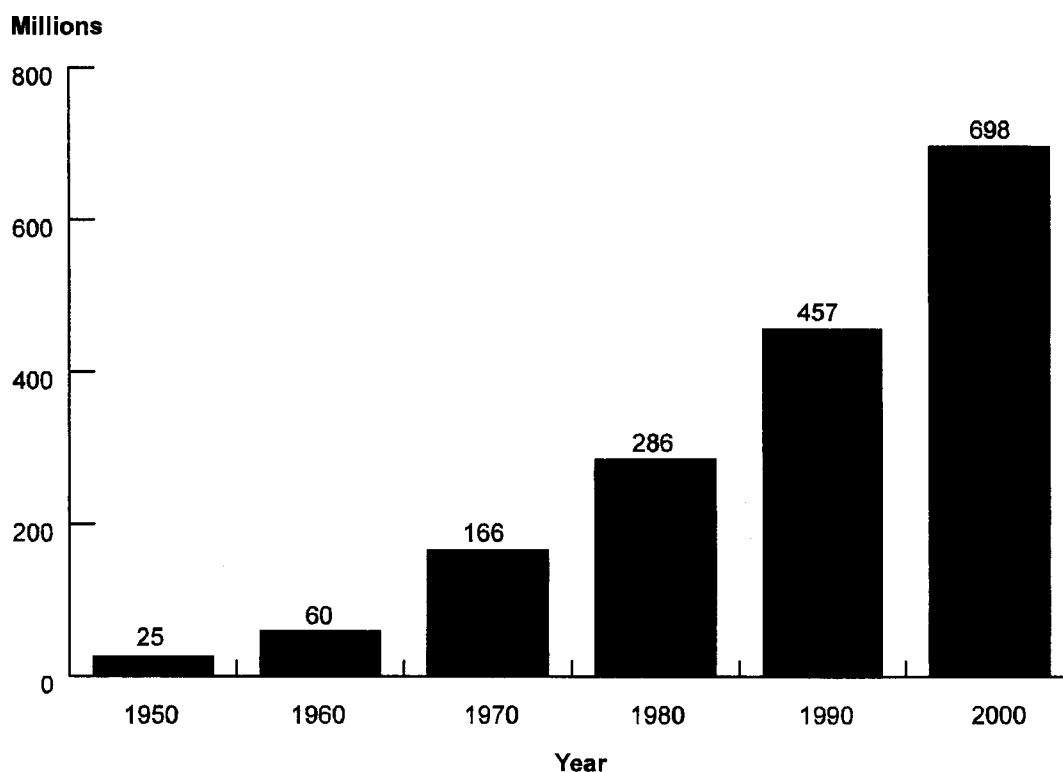
During the past 50 years, tourism has become the world's largest industry, with international tourist arrivals increasing from 25 million in 1950 to nearly 700 million in 2000 (fig.4) (Bridges et al. 2001).

The value of world trade in agricultural products has increased from approximately \$52 billion in 1970 to about \$417 billion in 1999

(Food and Agriculture Organization of the United Nations, n.d.). From 1989 to 1999, the volume of livestock and livestock-product exports (other than sheep, goats, and wool) has risen at annual rates ranging from a low of 0.25 percent for ovine meat to a high of more than 14 percent for poultry meat, while dairy products and pork have increased annually by nearly 5 percent and 6 percent, respectively (Upton 2001).

Figure 4—Trend in world travel international tourist arrivals*, 1950–2000. (*Adapted from Bridges et al 2001; source: World Tourism Organization*).

International Tourist Arrivals



*Same-day visitors excluded

Breakdowns in public- and animal-health measures—In some parts of the world, the breakdowns of human- and animal-health measures—and the lack of adequate veterinary infrastructure—have had major impacts on disease emergence and transmission. A government's inability to enforce sanitary regulations or to provide needed vaccines and medications contributes to disease transmission. For example, the lack of funds for vaccines has led to the recent resurgence of FMD in several African countries. In addition, slaughtering unhealthy food animals under unhygienic conditions can lead to the spread of zoonotic diseases.

Poverty and social inequality—Lower socioeconomic status is associated with greater infectious disease burden due to poor living conditions, the inability to afford health care, and other factors. Unhealthy populations also exert a negative impact on economic productivity.

War and famine—War, famine, and political upheaval lead to many factors associated with disease emergence, such as migration of people and animals, breakdowns of public- and animal-health measures, increased susceptibility to infection, and poverty. For example, political upheaval in Zimbabwe led to the spread of livestock animal disease. During the upheaval, there was no control over animal movement, animals were unattended, and neither the government nor livestock owners had money to buy vaccines.

Lack of political resolve—To prevent and control infectious disease, governments, corporations, health professionals, and private citizens must work together and have the political resolve to accomplish the task.

Intent to harm—Terrorist attacks with biological weapons could lead to the emergence of disease in human and animal populations. The intent to harm may spur the creation of more deadly disease agents through biotechnology.

While predicting the time and place of the emergence of a new disease presents many challenges, a qualitative estimate or ranking of the risk potential or vulnerability for an emerging disease might be made by evaluating the above factors at varying geographic levels, such as global region, country, or subcountry. Another approach is to evaluate the characteristics and practices of a country's individual livestock industries, according to their potential for disease emergence. Important questions include:

- Is production moving into new areas?
- Are imports and exports changing?
- Are new production systems being used?
- What is the degree of interaction between domestic and wild animals?
- Are there adequate regulatory and biosecurity safeguards?
- Are identified changes or trends in the industry moving in the direction of less disease-emergence potential or more disease-emergence potential?

Answers to these questions could help identify the degree of risk for emerging disease in a livestock industry and highlight areas where preventive measures could be taken. For example, the Agriculture Disaster Research Institute RoadMap project has identified the

characteristics and practices of the U.S. swine industry; simulated an outbreak situation; and identified gaps and vulnerabilities in the pork food chain. The project will develop strategies to address gaps and vulnerabilities (Slenning 2004).

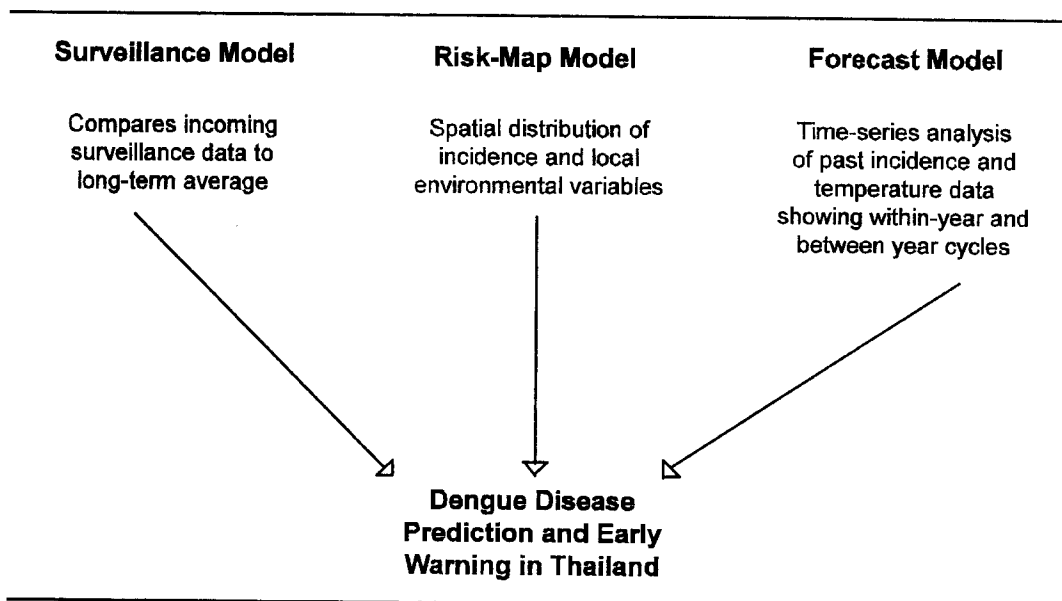
EARLY WARNING SYSTEMS

Epidemic prevention and control activities can be initiated by monitoring a wide range of indicators, from simple surveillance and early reporting of outbreak detection to complex forecasting models. These various indicators can be arranged in a hierarchical system known as an Early Warning System (EWS).

For example, in Thailand an extensive EWS is being created for the endemic mosquito-borne disease dengue fever. The dengue EWS is comprised of a surveillance model, a risk-map model, and a forecasting model (fig. 5). The surveillance model plots incoming surveillance case data against the long-term average for that

month. Case numbers that exceed 2 standard deviations from normal are considered cause for concern. The risk-map model shows the spatial distribution of incidence rates by administrative units combined with satellite data on important environmental variables related to local variation in risk. The forecasting model is based on time-series analysis of past case numbers combined with temperature data showing within-year cycles and between-year cycles. The three model components are projected into the future to make disease predictions, and this information can be used by decisionmakers to coordinate disease control programs (Myers et al. 2000).

Figure 5—Dengue EWS for Thailand. (*Adapted from Myers et al. 2000*)



The Famine Early Warning System (FEWS) Network is another example of a successful, formalized EWS. Although the targeted outcome is famine and not an infectious disease, FEWS has many similarities to an infectious-disease EWS. FEWS is a specialized information network designed to enhance the abilities of African countries and regional organizations to manage the risk of food insecurity through timely and analytical early warning and vulnerability information.

FEWS is a partnership-based program developed and funded in the late 1980s by the U.S. Agency for International Development. Information in the network (see <http://www.fews.net>) includes satellite data for early identification of drought and other weather conditions, such as floods and cyclones; and local ground-based information on health,

conflict, or other factors affecting access to food, types of crops farmers are planting, food prices at regional markets, and the extent of malnutrition and HIV/acquired immunodeficiency syndrome. The analytical framework used includes a baseline analysis of internal vulnerability (normal sources of food and income) combined with an analysis of external hazards (drought, flood, change in crop production, etc.) to provide an analysis of risk of food shortage (outcome). This information is provided to decisionmakers who can then take early action to prevent famine. Timely and accurate information about food security conditions is also disseminated to the general public and the media. FEWS has been successful in preventing serious droughts from becoming famines in the Sahel, southern Africa, and Ethiopia through early warning and early public action.

CONCLUSION

There is a wide variety of methods to predict and model infectious-disease emergence. Choosing the appropriate model type depends on the objectives and the questions to be answered, the data that are available, and the target audience for the model. Before decisions are made based on model results, the limitations

of the model must be considered. Models are inherently a simplification of a real situation and are often developed with imperfect data. Nevertheless, models can improve our understanding of the emergence of infectious diseases, assist in planning disease surveillance and control strategies, and potentially prevent epidemics.

APPENDIX I: REFERENCES CITED

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APPENDIX II: BACKGROUND SOURCES

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